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BD015361
LOCUS          BD015361             822 bp      DNA      linear      PAT 27-AUG-2002
DEFINITION    Human protein and cDNA[4].
ACCESSION     BD015361
VERSION       BD015361.1 GI:22556499
KEYWORDS      JP 2001218584-A/7.
SOURCE        Homo sapiens (human)
ORGANISM      Homo sapiens
              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
              Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE     1 (bases 1 to 822)
AUTHORS       Kato, S. and Saeki, M.
TITLE         Human protein and cDNA[4]
JOURNAL       JAPAN SCIENCE AND TECHNOLOGY CORP
COMMENT       OS Homo sapiens (human)
              PN JP 2001218584-A/7
              PD 14-AUG-2001
              PF 08-FEB-2000 JP 2000031062
              PI SEIJI KATO,MIHORO SAEKI
              PC C12N15/09,C07K14/435,C07K16/18,C12N1/15,C12N1/19,C12N1/21, PC
              C12N5/10//
              CC C12P21/08,C12N15/00,C12N5/00
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              FT CDS Location/Qualifiers
              source
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              /organism="Homo sapiens"
              /mol_type="genomic DNA"
              /db_xref="taxon:9606"
BASE COUNT    210 a 186 c 199 g 227 t
ORIGIN
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Pred. No.:    9,12e-69      Length:    822
Score:        918.00      Matches:    178
Percent Similarity: 100.00%      Conservative: 0
Best Local Similarity: 100.00%      Mismatches: 0
Query Match:  100.00%      Indels:    0
DB:           6           Gaps:      0

US-10-029-137-2 (1-178) x BD015361 (1-822)

Qy 1 MetAlaAlaProLeuGlyGlyMetPheSerGlyGlnProGlyProGlnAlaPro 20
Db 10 ATGGCGGCTCCACTAGGGGGTATGTTTCTGGGAGCACCACCGCTCCGCTCAGGCCCG 69
Qy 21 ProGlyLeuProGlyGlnAlaSerLeuGlnAlaAlaProGlyAlaProArgProSer 40
Db 70 CCGGGCCCTTCGGGGCCAAAGCTTCGCTTCTTCAGGAGCTCCAGGCGCTCCAGACCTTCC 129
Qy 41 SerSerThrLeuValAspGluLeuGluSerPheGluAlaCysPheAlaSerLeuVal 60
Db 130 AGCAGTACTTTGGTGGAGCTGGAGTTCATCTTCGAGGCTTCGTCATCTCTGGTG 199
Qy 61 SerGlnAspTyrValAsnGlyThrAspGlnGluLulleArgThrGlyValAspGlnCys 80
Db 190 AGTCAGGACTATGTCATTAATGGCCAGCTTCAGGAAGAAATTCGAACCGGTGTTCAGTGT 249
Qy 81 IleGlnLysPheLeuAspIleAlaArgGlnThrGluCysPhePheLeuGlnLysArgLeu 100
Db 250 ATCCAGAGTTTCTGGATATTCCAGACAGACAGAAATGTTTTTCTTACAAAAGATTG 309
Qy 101 GlnLeuSerValGlnLysProGlnGlnValIleLysGluAspValSerGluLeuArgAsn 120
Db 310 CAGTTATCTGTCAGAAACCCAGCAAGTATCAAAAGAGGATGTGTCAAGAACTAAGGAAT 369
Qy 121 GluLeuGlnArgLysAspAlaLeuValGlnLysHisLeuThrLysLeuArgHisTrpGln 140
Db 370 GAATTACAGCGGAAGATGCATAGTCCAGAAAGCACTTGACAAAGCTGAGGCAATTGGCAG 429
Qy 141 GlnValLeuGluAspIleAsnValGlnHisLysLysProAlaAspIleProGlnGlySer 160

430 CAGGTCTGGAGACATCAAGTGCAGCACAACCAAGCCCGCAGCATCCCTCAGGGGTCC 489
161 LeuAlaTyrLeuGluGlnAlaSerAlaAsnIleProAlaProLeuLysProThr 178
490 TTGGCTTACTTGGAGCAGCATCTGCCAACATCCTCGACCTCTGAAGCCCAAG 543

RESULT 2
AX014817
LOCUS          AX014817             882 bp      DNA      linear      PAT 07-SEP-2000
DEFINITION    Sequence 3 from Patent WO9953040.
ACCESSION     AX014817
VERSION       AX014817.1 GI:10041084
KEYWORDS
SOURCE        Homo sapiens (human)
ORGANISM      Homo sapiens
              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
              Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE     1
AUTHORS       Schmitt,A., Specht,T., Dahl,E., Hinzmann,B., Rosenthal,A. and
              Pilarsky,C.
TITLE         Human nucleic acid sequences from ovarian tumour tissue
JOURNAL       Patent: WO 9953040-A 3 21-OCT-1999;
              SCHMITT ARMIN (DE); SPECHT THOMAS (DE); DAHL EDGAR (DE); HINZMANN
              BERND (DE); ROSENTHAL ANDRE (DE); METAGEN GRS PUER GENOMPORSCHUN
              (DE); PILARSKY CHRISTIAN (DE)
FEATURES      Location/Qualifiers
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              /mol_type="genomic DNA"
              /db_xref="taxon:9606"
BASE COUNT    238 a 190 c 206 g 248 t
ORIGIN
Alignment Scores:
Pred. No.:    9,95e-69      Length:    882
Score:        918.00      Matches:    178
Percent Similarity: 100.00%      Conservative: 0
Best Local Similarity: 100.00%      Mismatches: 0
Query Match:  100.00%      Indels:    0
DB:           6           Gaps:      0

US-10-029-137-2 (1-178) x AX014817 (1-882)

Qy 1 MetAlaAlaProLeuGlyGlyMetPheSerGlyGlnProGlyProGlnAlaPro 20
Db 10 ATGGCGGCTCCACTAGGGGGTATGTTTCTGGGAGCACCACCGCTCCGCTCAGGCCCG 69
Qy 21 ProGlyLeuProGlyGlnAlaSerLeuGlnAlaAlaProGlyAlaProArgProSer 40
Db 70 CCGGGCCCTTCGGGGCCAAAGCTTCGCTTCTTCAGGAGCTCCAGGCGCTCCAGACCTTCC 129
Qy 41 SerSerThrLeuValAspGluLeuGluSerPheGluAlaCysPheAlaSerLeuVal 60
Db 130 AGCAGTACTTTGGTGGAGCTGGAGTTCATCTTCGAGGCTTCGTCATCTCTGGTG 189
Qy 61 SerGlnAspTyrValAsnGlyThrAspGlnGluLulleArgThrGlyValAspGlnCys 80
Db 190 AGTCAGGACTATGTCATTAATGGCCAGCTTCAGGAAGAAATTCGAACCGGTGTTCAGTGT 249
Qy 81 IleGlnLysPheLeuAspIleAlaArgGlnThrGluCysPhePheLeuGlnLysArgLeu 100
Db 250 ATCCAGAGTTTCTGGATATTCCAGACAGACAGAAATGTTTTTCTTACAAAAGATTG 309
Qy 101 GlnLeuSerValGlnLysProGlnGlnValIleLysGluAspValSerGluLeuArgAsn 120
Db 310 CAGTTATCTGTCAGAAACCCAGCAAGTATCAAAAGAGGATGTGTCAAGAACTAAGGAAT 369
Qy 121 GluLeuGlnArgLysAspAlaLeuValGlnLysHisLeuThrLysLeuArgHisTrpGln 140
Db 370 GAATTACAGCGGAAGATGCATAGTCCAGAAAGCACTTGACAAAGCTGAGGCAATTGGCAG 429
Qy 141 GlnValLeuGluAspIleAsnValGlnHisLysLysProAlaAspIleProGlnGlySer 160

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